



Introduction to the SAMPREP special issue

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Sample quality is of foundational importance to structural biology. Yet, detailed cross-disciplinary best practices are rarely consolidated into a single forum. The SAMPREP (Sample Attributes for Multiple-techniques and Principal Requirements for Experiments in Pan-structural biology) workshop, convened at the 2023 ACA Annual Meeting in Baltimore, was designed to address this need. Organized by nine experts representing major synchrotrons, cryo-EM, crystallization and structural biology cores, the one-day program assembled 22 participants for a series of sessions focused on practical approaches to sample preparation and handling.

The day began with talks on protein purification and sample-quality evaluation from James Byrnes (Brookhaven National Laboratory) and Marco Mazzorana (Diamond Light Source). This was followed by presentations on solution-based methods: Thomas Weiss (SLAC) discussed considerations for SAXS experiments, Kushol Gupta (University of Pennsylvania) highlighted complementary biophysical techniques for evaluating sample suitability, and Ligu Wang (Brookhaven) together with Christina Zimanyi (New York Structural Biology Center) provided guidance on preparing samples for cryo-electron microscopy. At lunch, Stephen Maughan (Refeyn) introduced the emerging technology of mass photometry.

In the afternoon, Sarah Bowman (University of Buffalo Hauptman–Woodward Medical Research Institute) and Vivian Stojanoff (Brookhaven) shared strategies for successful crystallization, while Silvia Russi (SLAC), along with Byrnes, Bowman and Zimanyi, led a session on transporting samples safely to facilities, covering shipping at 4°C, handling dry-shipping dewars and other logistical challenges. The program also featured a case study from Max Watkins (BioCAT, APS), who illustrated the integration of SAXS and cryo-EM in studying the conformational dynamics of cobalamin-dependent methionine synthase (Watkins *et al.*, 2023). The day concluded with an open forum where attendees engaged directly with the instructors, asking questions that spanned crystallization of co-complexes, cryoprotection strategies, analysis of antibody–antigen samples and best practices for handling glycosylated proteins.

This special issue of *Acta Crystallographica Section F* builds upon the workshop's major themes, featuring three contributions:

Cryo-EM sample preparation for high-resolution structure studies (Wang & Zimanyi, 2024). This article provides a clear roadmap for preparing cryo-EM samples that are optimized for achieving high-resolution reconstructions. The authors discuss practical aspects of buffer selection, concentration ranges and strategies for troubleshooting issues such as aggregation, preferred orientation and other artifacts. The paper emphasizes how subtle differences in vitrification or biochemical preparation can directly influence the quality of cryo-EM data, offering concrete tips that will be valuable for both novice and experienced practitioners.

Preparing research samples for safe arrival at centers and facilities: recipes for successful experiments (Bowman *et al.*, 2024). This article addresses an often-overlooked but critical element of structural biology research: the logistics of transporting samples from home laboratory to national facilities. The authors provide detailed guidance on packing and shipping strategies, including temperature control (*e.g.* maintaining at 4°C or cryogenic conditions), labeling and compliance with carrier and facility requirements. Their advice extends to handling specialized containers such as dry-shipping dewars, as well as common pitfalls encountered during transit. By focusing on this practical aspect of experimental workflows, the paper fills an important gap that directly affects the success of data collection at user facilities.

Preparing for successful protein crystallization experiments (Budziszewski *et al.*, 2025). This contribution approaches one of the most enduring challenges in structural biology: obtaining well ordered crystals of macromolecules. The authors discuss biochemical and physical considerations, review different methods for crystallization and present strategies for optimizing buffer systems, additives and protein constructs, highlighting approaches for troubleshooting crystallization failures. Importantly, the article emphasizes reproducibility and consistency, illustrating how careful attention to sample preparation can significantly increase the likelihood of generating crystals suitable for diffraction experiments. With a forward-looking perspective, the discussion is enriched with examples from high-throughput crystallization pipelines, providing guidance that can be scaled from small academic laboratories to large facilities.

Together, these articles provide a unified set of guidelines that extend the workshop's impact. By marrying method-specific expertise with practical logistics, they provide a durable resource for the community and reinforce the central role of thoughtful sample preparation in ensuring success across the diverse experimental landscape of structural biology. The workshop and these articles together bridge

communities that often work in parallel rather than in concert. This special issue distills experience from multiple disciplines into actionable guidance. It is hoped that these contributions will not only support individual researchers in their daily practice but also encourage a culture of preparation and collaboration that strengthens the entire structural biology community.

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